

ABSTRACT

Methods and kits for classifying patients having diffuse large B-cell lymphoma (DLBCL) based upon expression of a plurality of genes are disclosed. Real-time quantitative RT-PCR can be used to measure expression values. Correlating expression values of the plurality of genes in a tumor sample from the patient to reference expression values obtained from DLBCL patients can stratify patients in the classification groups. The methods and kits can be used to predict overall patient survival.